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INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification <sup>6</sup> : <b>C12Q 1/68</b>	<b>A1</b>	(11) International Publication Number: <b>WO 98/41657</b> (43) International Publication Date: 24 September 1998 (24.09.98)													
<p>(21) International Application Number: PCT/US98/05451</p> <p>(22) International Filing Date: 19 March 1998 (19.03.98)</p> <p>(30) Priority Data:</p> <table border="0"> <tr> <td>60/041,435</td> <td>20 March 1997 (20.03.97)</td> <td>US</td> </tr> <tr> <td>60/073,853</td> <td>2 February 1998 (02.02.98)</td> <td>US</td> </tr> </table> <p>(63) Related by Continuation (CON) or Continuation-in-Part (CIP) to Earlier Applications</p> <table border="0"> <tr> <td>US</td> <td>60/041,435 (CIP)</td> </tr> <tr> <td>Filed on</td> <td>20 March 1997 (20.03.97)</td> </tr> <tr> <td>US</td> <td>60/073,853 (CIP)</td> </tr> <tr> <td>Filed on</td> <td>2 February 1998 (02.02.98)</td> </tr> </table> <p>(71) Applicant (for all designated States except US): AFFYMETRIX, INC. [US/US]; 3380 Central Expressway, Santa Clara, CA 95051 (US).</p> <p>(72) Inventor; and (75) Inventor/Applicant (for US only): CHEE, Mark [AU/US]; 3199 Waverly Street, Palo Alto, CA 94306 (US).</p>	60/041,435	20 March 1997 (20.03.97)	US	60/073,853	2 February 1998 (02.02.98)	US	US	60/041,435 (CIP)	Filed on	20 March 1997 (20.03.97)	US	60/073,853 (CIP)	Filed on	2 February 1998 (02.02.98)	<p>(74) Agents: LIEBESCHUETZ, Joe et al.; Townsend and Townsend and Crew LLP, 8th floor, Two Embarcadero Center, San Francisco, CA 94111-3834 (US).</p> <p>(81) Designated States: JP, US, European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE).</p> <p><b>Published</b> <i>With international search report.</i></p>
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<p>(54) Title: ITERATIVE RESEQUENCING</p> <p>(57) Abstract</p> <p>The invention provides iterative methods of analyzing a target nucleic acid that represents a variant of a reference nucleic acid. An array of probes is designed to be complementary to an estimated sequence of a target nucleic acid. The array of probes is then hybridized to the target nucleic acid. The target sequence is reestimated from hybridization pattern of the array to the target nucleic acid. A further array of probes is then designed to be complementary to the reestimated sequence, and this array is used to obtain a further reestimate of the sequence of the target nucleic acid. By performing iterative cycles of array design and target sequence estimation, the estimated sequence of the target converges with the true sequence.</p>															

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